GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 10, 2006, 16:29:52 ; Search time 18 Seconds
(without alignments)
248.599 Million cell updates/sec

Title: US-10-613-076-48
Perfect score: 1857
Sequence: 1 MPGWLTLPTLCRFLLWAFTI.........FGFPRPQQAAYGXXCYABNX 341

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 97014 seqs, 13112538 residues

Total number of hits satisfying chosen parameters: 97014

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA New:*
1: /cgn2_6/ptcdata/1/pubpaa/US08_NEW_PUB.pep:*
2: /cgn2_6/ptcdata/1/pubpaa/US06_NEW_PUB.pep:*
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6: /cgn2_6/ptcdata/1/pubpaa/US10_NEW_PUB.pep:*
7: /cgn2_6/ptcdata/1/pubpaa/US11_NEW_PUB.pep:*
8: /cgn2_6/ptcdata/1/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the total score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	744.5	40.1	402	7	US-11-174-150-47	Sequence 47, Appl
2	189.5	10.2	457	6	US-10-986-501-110	Sequence 110, App
3	180.5	9.2	2439	7	US-11-128-059-76	Sequence 76, Appl
4	173.5	9.3	721	7	US-11-128-059-88	Sequence 88, Appl
5	173.5	9.3	897	6	US-10-453-372-208	Sequence 208, App
6	173.5	9.3	931	7	US-11-128-059-86	Sequence 86, Appl
7	173.5	9.3	1323	7	US-11-128-059-92	Sequence 92, Appl
8	173.5	9.3	1327	7	US-11-128-059-84	Sequence 84, Appl
9	173.5	9.3	1416	7	US-11-128-059-4	Sequence 4, Appli
10	173.5	9.3	1502	6	US-10-453-372-252	Sequence 252, App
11	173.5	9.3	1510	6	US-10-453-372-254	Sequence 254, App
12	173.5	9.3	2458	7	US-11-128-059-94	Sequence 94, Appl
13	173.5	9.3	2551	6	US-10-453-372-256	Sequence 256, App
14	173.5	9.3	2551	7	US-11-128-059-96	Sequence 96, Appl
15	173	9.3	353	7	US-11-128-059-90	Sequence 90, Appl
16	171	9.2	315	6	US-10-453-372-212	Sequence 212, App
17	170	9.2	533	6	US-10-453-372-230	Sequence 230, App
18	170	9.2	533	6	US-10-453-372-232	Sequence 232, App
19	170	9.2	552	6	US-10-453-372-236	Sequence 236, App
20	170	9.2	552	6	US-10-453-372-238	Sequence 238, App
21	170	9.2	552	6	US-10-453-372-240	Sequence 240, App
22	170	9.2	552	6	US-10-453-372-242	Sequence 242, App
23	170	9.2	552	6	US-10-453-372-246	Sequence 246, App
24	170	9.2	552	6	US-10-453-372-250	Sequence 250, App
25	170	9.2	556	6	US-10-453-372-210	Sequence 210, App
26	170	9.2	2313	7	US-11-128-059-80	Sequence 80, Appl
27	170	9.2	2358	7	US-11-128-059-74	Sequence 74, Appl
28	170	9.2	2417	6	US-10-453-372-228	Sequence 228, App
29	169.5	9.1	93	7	US-11-128-059-5	Sequence 5, Appli
30	169	9.1	552	6	US-10-453-372-234	Sequence 234, App
31	167	9.0	552	6	US-10-453-372-248	Sequence 248, App
32	166	8.9	1431	7	US-11-128-059-2	Sequence 2, Appli
33	164	8.8	552	6	US-10-453-372-244	Sequence 244, App
34	130.5	7.0	92	7	US-11-128-059-70	Sequence 70, Appl
35	111.5	6.0	124	7	US-11-128-059-64	Sequence 64, Appl
36	110	5.9	322	6	US-10-063-703-6	Sequence 6, Appli
37	110	5.9	322	7	US-11-102-240-6	Sequence 6, Appli
38	106.5	5.7	111	7	US-11-155-775-36	Sequence 36, Appl
39	104.5	5.6	98	7	US-11-084-554-219	Sequence 219, App
40	104.5	5.6	98	7	US-11-136-250-219	Sequence 219, App
41	104	5.6	250	7	US-11-054-515-1529	Sequence 1529, Ap
42	103.5	5.6	7968	7	US-11-186-731-5	Sequence 5, Appli
43	102.5	5.5	99	7	US-11-084-554-221	Sequence 221, App
44	102.5	5.5	99	7	US-11-136-250-221	Sequence 221, App
45	102	5.5	4346	6	US-10-995-561-671	Sequence 671, App

ALIGNMENTS

RESULT 1
US-11-174-150-47
; Sequence 47, Application US/11174150
; Publication No. US20050260714A1
; GENERAL INFORMATION:
; APPLICANT: Agarwal, Pankaj
; APPLICANT: Murdoch, Paul R.
; APPLICANT: Rizvi, Safia K.
; APPLICANT: Smith, Randall F.
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP50022
; CURRENT APPLICATION NUMBER: US/11/174,150
; CURRENT FILING DATE: 2005-07-01
; PRIOR APPLICATION NUMBER: US/10/257,174
; PRIOR APPLICATION FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: PCT/US01/11797
; PRIOR APPLICATION FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 60/196,603
; PRIOR FILING DATE: 2000-04-13
; PRIOR APPLICATION NUMBER: 60/199,417
; PRIOR FILING DATE: 2000-04-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 47
; LENGTH: 402
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-174-150-47

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Best Local Similarity 46.2%; Pred. No. 1.2e-60;
Matches 158; Conservative 43; Mismatches 104; Indels 37; Gaps 9;

Qy 20 IFHKAQGDPAS------HPGPHYLLPPIHEVIHSHRGATATLPCVLGTTPPSY----KVR 69
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Db 36 VVHVLEGSGSVVVQTAPGQ--------VVSHRGGTIVLPCRYHYEAAAHGHDGVRLK 85

Qy 70 WSK-VEPGLRETLILITNGLHARGYGPLGGRARMRGRHRLDASLVIAGVRLEDEGRYRC 128
    |:|:| |||| |:||:| |:| ||
Db 86 WTKVVDP--LAFTDVFVALGPQHRAFGSYRGRAELQGDGPGDASLVLRNVTLQDYGRYEC 143

Qy 129 ELNGIEDRSVALTLSLEGVVFPVQPSRGRYQFNYYEAKQACEEQDGRLATYSQLYQAWT 188
   |:| |:: : ||| |: | |:| |||
Db 144 EVTNELEDDAGMVKLDLRGVVFPYHPRGGRYKLTFAEAQRACAEQDGIIASAEQLHAAWR 203

Qy 189 EGLDWCNAGWLLEGSVRYPVLTARAPCGRG-----------RPGIRSYGPRDRMRDRYD 237
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                    GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on:      February 10, 2006, 16:28:10 ; Search time 48 Seconds
                           (without alignments)
                           587.342 Million cell updates/sec

Title:           US-10-613-076-48
Perfect score:   1857
Sequence:        1 MPGWLTLTPLCRFLLWAFTI.........FGFPRPQQAAYGXXCYABNX 341

Scoring table:   BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched:        572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters:      572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :    Issued_Patents AA:*
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        3: /cgm2_6/ptodata/1/iaa/H_COMB.pep:*
        4: /cgm2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
        5: /cgm2_6/ptodata/1/iaa/RB_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	857.5	46.2	360	2	US-09-907-794A-213	Sequence 213, App
2	857.5	46.2	360	2	US-09-905-125A-213	Sequence 213, App
3	857.5	46.2	360	2	US-09-902-775A-213	Sequence 213, App
4	857.5	46.2	360	2	US-09-906-700-213	Sequence 213, App
5	857.5	46.2	360	2	US-09-903-603A-213	Sequence 213, App
6	857.5	46.2	360	2	US-09-904-920A-213	Sequence 213, App
7	857.5	46.2	360	2	US-09-909-064-213	Sequence 213, App
8	897.5	46.2	360	2	US-09-905-381A-213	Sequence 213, App
9	857.5	46.2	360	2	US-09-906-618-213	Sequence 213, App
10	857.5	46.2	360	2	US-09-906-646-213	Sequence 213, App
11	857.5	46.2	360	2	US-09-904-462-213	Sequence 213, App
12	857.5	46.2	360	2	US-09-902-736A-213	Sequence 213, App
13	857.5	46.2	360	2	US-09-906-722A-213	Sequence 213, App
14	811.5	43.7	373	2	US-09-949-016-10485	Sequence 10485, A
15	799	43.0	355	2	US-09-466-778-9	Sequence 9, Appli
16	772	41.6	326	4	US-08-225-477B-6	Sequence 6, Appli
17	772	41.6	326	4	PCT-US95-04353-6	Sequence 6, Appli
18	576.5	31.0	1257	1	US-08-340-428B-49	Sequence 49, Appl
19	565	30.4	333	4	US-08-225-477B-4	Sequence 4, Appli
20	565	30.4	333	4	PCT-US95-04353-4	Sequence 4, Appli
21	564	30.4	289	2	US-09-466-778-8	Sequence 8, Appli
22	550	29.6	912	2	PCT-US95-03747-2	Sequence 2, Appli
23	546.5	29.4	378	4	US-08-225-477B-9	Sequence 9, Appli
24	546.5	29.4	378	4	PCT-US95-04353-9	Sequence 9, Appli
25	543	29.2	649	2	US-10-188-495-63	Sequence 63, Appl
26	543	29.2	671	2	US-09-799-118-61	Sequence 61, Appl
27	533	28.7	371	1	US-08-225-477B-8	Sequence 8, Appli
28	533	28.7	371	4	PCT-US95-04353-8	Sequence 8, Appli
29	529.5	28.5	883	2	US-10-195-970-3	Sequence 3, Appli
30	529.5	28.5	883	2	US-10-195-970-6	Sequence 6, Appli
31	528.5	28.5	883	2	US-10-188-495-72	Sequence 72, Appl
32	522	28.1	2316	2	US-09-949-002-314	Sequence 314, App
33	522	28.1	2415	2	US-09-949-002-398	Sequence 398, App
34	517	27.8	2409	6	5180808-2	Patent No. 5180808
35	506.5	27.3	328	4	US-08-225-477B-5	Sequence 5, Appli
36	506.5	27.3	328	4	PCT-US95-04353-5	Sequence 5, Appli
37	490	26.4	329	3	US-08-225-477B-3	Sequence 3, Appli
38	490	26.4	329	4	PCT-US95-04353-3	Sequence 3, Appli
39	403.5	21.7	908	4	PCT-US95-03747-3	Sequence 3, Appli
40	384.5	20.7	528	2	US-09-010-147B-20	Sequence 20, Appl
41	384.5	20.7	528	2	US-10-188-495-71	Sequence 71, Appl
42	338.5	18.2	98	1	US-08-242-097-4	Sequence 4, Appli
43	338.5	18.2	98	2	US-09-206-695-4	Sequence 4, Appli
44	338.5	18.2	98	2	US-09-799-118-4	Sequence 4, Appli
45	204.5	11.0	275	2	US-09-466-778-12	Sequence 12, Appl

ALIGNMENTS

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RESULT 1
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;  Sequence 213, Application US/09907794A
;  Patent No. 6635468
;  GENERAL INFORMATION:
;  APPLICANT: Genentech, Inc.
;  APPLICANT: Ashkenazi, Avi
;  APPLICANT: Botstein, David
;  APPLICANT: Desnoyers, Luc
;  APPLICANT: Eaton, Dan L.
;  APPLICANT: Ferrara, Napoleone
;  APPLICANT: Filvaroff, Ellen
;  APPLICANT: Fong, Sherman
;  APPLICANT: Gao, Wei-Qiang
;  APPLICANT: Gerber, Hanspeter
;  APPLICANT: Gerritsen, Mary E.
;  APPLICANT: Goddard, A.
;  APPLICANT: Godowski, Paul J.
;  APPLICANT: Grimaldi, Christopher J.
;  APPLICANT: Gurney, Austin L.
;  APPLICANT: Hillan, Kenneth, J.
;  APPLICANT: Kljavin, Ivar J.
;  APPLICANT: Mather, Jennie P.
;  APPLICANT: Pan, James
;  APPLICANT: Paoni, Nicholas F.
;  APPLICANT: Roy, Margaret Ann
;  APPLICANT: Stewart, Timothy A.
;  APPLICANT: Tumas, Daniel
;  APPLICANT: Williams, P. Mickey
;  APPLICANT: Wood, William, I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION: Acids Encoding the Same
;  FILE REFERENCE: 10466-14
;  CURRENT APPLICATION NUMBER: US/09/907,794A
;  CURRENT FILING DATE: 2001-07-17
;  PRIOR APPLICATION NUMBER: PCT/US00/04414
;  PRIOR FILING DATE: 2000-02-22
;  PRIOR APPLICATION NUMBER: US 60/143,048
;  PRIOR FILING DATE: 1999-07-07
;  PRIOR APPLICATION NUMBER: US 60/145,698
;  PRIOR FILING DATE: 1999-07-26
;  PRIOR APPLICATION NUMBER: US 60/146,222
;  PRIOR FILING DATE: 1999-07-28
;  PRIOR APPLICATION NUMBER: PCT/US99/20594
;  PRIOR FILING DATE: 1999-09-08
;  PRIOR APPLICATION NUMBER: PCT/US99/20944
;  PRIOR FILING DATE: 1999-09-13
;  PRIOR APPLICATION NUMBER: PCT/US99/21090
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/21547
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                     GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on:    February 10, 2006, 16:29:01 ; Search time 179 seconds
                                        (without alignments)
                                        -795.977 Million cell updates/sec

Title:          US-10-613-076-48
Perfect score:  1857
Sequence:       1 MPGWLTLPTLCRFLLWAFTI.........FGFPRPQQAAYGXXCYAENX 341

Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched:       1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters:       1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published Applications_AA_Main:*
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        3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
        4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
        5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
        6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                        SUMMARIES
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Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	1856	99.9	340	4	US-10-112-944-397	Sequence 397, App
2	1855	99.9	341	4	US-09-948-820-48	Sequence 48, Appl
3	1855	99.9	341	5	US-10-613-076-48	Sequence 48, Appl
4	1390	74.9	258	3	US-09-764-853-840	Sequence 840, App
5	1390	74.9	258	3	US-10-091-438-205	Sequence 205, App
6	1348	72.6	261	3	US-09-764-853-669	Sequence 669, App
7	1348	72.6	261	4	US-10-091-438-144	Sequence 144, App
8	857.5	46.2	360	3	US-09-909-320-213	Sequence 213, App
9	857.5	46.2	360	3	US-09-909-088B-213	Sequence 213, App
10	857.5	46.2	360	3	US-09-905-291A-213	Sequence 213, App
11	857.5	46.2	360	3	US-09-902-853-213	Sequence 213, App
12	857.5	46.2	360	3	US-09-907-824-213	Sequence 213, App
13	857.5	46.2	360	3	US-09-907-841-213	Sequence 213, App
14	857.5	46.2	360	3	US-09-904-011-213	Sequence 213, App
15	857.5	46.2	360	3	US-09-903-640-213	Sequence 213, App
16	857.5	46.2	360	3	US-09-908-093-213	Sequence 213, App
17	857.5	46.2	360	3	US-09-906-742-213	Sequence 213, App
18	857.5	46.2	360	3	US-09-906-838-213	Sequence 213, App
19	857.5	46.2	360	3	US-09-907-613-213	Sequence 213, App
20	857.5	46.2	360	3	US-09-907-942-213	Sequence 213, App
21	857.5	46.2	360	3	US-09-904-859-213	Sequence 213, App
22	857.5	46.2	360	3	US-09-909-204-213	Sequence 213, App
23	857.5	46.2	360	3	US-09-904-820-213	Sequence 213, App
24	857.5	46.2	360	3	US-09-904-786-213	Sequence 213, App
25	857.5	46.2	360	3	US-09-906-646-213	Sequence 213, App
26	857.5	46.2	360	3	US-09-906-700-213	Sequence 213, App
27	857.5	46.2	360	3	US-09-903-786-213	Sequence 213, App
28	857.5	46.2	360	3	US-09-902-903-213	Sequence 213, App
29	857.5	46.2	360	3	US-09-903-749A-213	Sequence 213, App
30	857.5	46.2	360	3	US-09-904-119-213	Sequence 213, App
31	857.5	46.2	360	3	US-09-904-956-213	Sequence 213, App
32	857.5	46.2	360	3	US-09-902-736-213	Sequence 213, App
33	857.5	46.2	360	3	US-09-907-794-213	Sequence 213, App
34	857.5	46.2	360	3	US-09-903-943-213	Sequence 213, App
35	857.5	46.2	360	3	US-09-904-462-213	Sequence 213, App
36	857.5	46.2	360	3	US-09-907-925-213	Sequence 213, App
37	857.5	46.2	360	3	US-09-902-692-213	Sequence 213, App
38	857.5	46.2	360	3	US-09-903-520-213	Sequence 213, App
39	857.5	46.2	360	3	US-09-905-056-213	Sequence 213, App
40	857.5	46.2	360	3	US-09-909-064-213	Sequence 213, App
41	857.5	46.2	360	3	US-09-904-553-213	Sequence 213, App
42	857.5	46.2	360	3	US-09-905-381-213	Sequence 213, App
43	857.5	46.2	360	3	US-09-904-485-213	Sequence 213, App
44	857.5	46.2	360	3	US-09-905-348-213	Sequence 213, App
45	857.5	46.2	360	3	US-09-905-088-213	Sequence 213, App

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                        ALIGNMENTS

RESULT 1
US-10-112-944-397
; Sequence 397, Application US/10112944
; Publication No. US20040048249A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Yang, Yonghong
; APPLICANT: Weng, Gezhi
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Xue, Aidong J.
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Wehrman, Tom
; APPLICANT: Ghosh, Malabika
; APPLICANT: Wang, Dunrui
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wang, Zhiwei
; TITLE OF INVENTION: No. US20040048249A1el Nucleic Acids and
; TITLE OF INVENTION:  Secreted Polypeptides
; FILE REFERENCE: 805A
; CURRENT APPLICATION NUMBER: US/10/112,944
; CURRENT FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US 09/488,725
; PRIOR APPLICATION FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: US 09/496,914
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: US 09/515,126
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: US 09/519,705
; PRIOR FILING DATE: 2000-03-07
; PRIOR APPLICATION NUMBER: US 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: US 09/552,929
; PRIOR FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: US 09/577,408
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 924
; SOFTWARE: pt_FL_genes Version 5.0
; SEQ ID NO 397
; LENGTH: 340
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-112-944-397

Query Match          99.9%;   Score 1856;  DB 4;  Length 340;
Best Local Similarity 99.4%;  Pred. No. 1.1e-152;
Matches 338; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 10, 2006, 16:19:59 ; Search time 203 Seconds
(without alignments)
738.070 Million cell updates/sec

Title: US-10-613-076-48
Perfect score: 1857
Sequence: 1 MPGWLTLPTLCRFLLWAFTI.........FGFPRPQQAAYGXXCYAENX 341

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21:*
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2: geneseqp1990s:*
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4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Match Length	DB	ID	Description
1	1856	99.9	340	8	ADM87304	Adm87304 Human pro
2	1856	99.9	343	6	ABU11635	Abu11635 Human MDD
3	1855	99.9	341	3	AAB12304	Aab12304 Human sec
4	1390	74.9	258	4	AAU18060	Aau18060 Human imm
5	1390	74.9	258	5	ABB10532	Abb10532 Human cDN
6	1390	74.9	258	5	ABP67119	Abp67119 Human pol
7	1390	74.9	258	7	ADB31684	Adb31684 Human nov
8	1348	72.6	261	4	AAU17999	Aau17999 Human imm
9	1348	72.6	261	4	ABB10361	Abb10361 Human cDN
10	1348	72.6	261	5	ABP66948	Abp66948 Human pol
11	1348	72.6	261	7	ADB31623	Adb31623 Human nov
12	1052	56.7	191	8	ADP71273	Adp71273 Human LP2
13	857.5	46.2	360	3	AAY13381	Aay13381 Amino aci
14	857.5	46.2	360	2	ADC78533	Adc78533 Human PRO
15	857.5	46.2	360	4	AAB80249	Aab80249 Human PRO
16	857.5	46.2	360	4	AAU29037	Aau29037 Human PRO
17	857.5	46.2	360	4	AAM38965	Aam38965 Human pol
18	857.5	46.2	360	6	ABU58413	Abu58413 Human PRO
19	857.5	46.2	360	6	ABU71627	Abu71627 Human PRO
20	857.5	46.2	360	6	ABU87961	Abu87961 Novel hum
21	857.5	46.2	360	6	ABU84276	Abu84276 Human sec
22	857.5	46.2	360	6	ABR66150	Abr66150 Human sec
23	857.5	46.2	360	6	ABR65540	Abr65540 Human sec
24	857.5	46.2	360	6	ABU99480	Abu99480 Human sec
25	857.5	46.2	360	6	ABU82719	Abu82719 Human PRO
26	857.5	46.2	360	6	ABU89840	Abu89840 Novel hum
27	857.5	46.2	360	6	ABU71482	Abu71482 Human PRO
28	857.5	46.2	360	6	ABR68089	Abr68089 Human sec
29	857.5	46.2	360	6	ABU96142	Abu96142 Novel hum
30	857.5	46.2	360	6	ABU92573	Abu92573 Human sec
31	857.5	46.2	360	6	ABO08650	Abo08650 Human sec
32	857.5	46.2	360	6	ABO02702	Abo02702 Human sec
33	857.5	46.2	360	6	ABR74856	Abr74856 Human sec
34	857.5	46.2	360	6	ABR94618	Abr94618 Human sec
35	857.5	46.2	360	6	ABU85591	Abu85591 Human PRO
36	857.5	46.2	360	6	ABU98751	Abu98751 Novel hum
37	857.5	46.2	360	6	ABU97966	Abu97966 Novel hum
38	857.5	46.2	360	6	ABU91672	Abu91672 Novel hum
39	857.5	46.2	360	6	ABU71928	Abu71928 Human sec
40	857.5	46.2	360	6	ABU89365	Abu89365 Human PRO
41	857.5	46.2	360	6	ABU86206	Abu86206 Human sec
42	857.5	46.2	360	6	ABU67419	Abu67419 Human sec
43	857.5	46.2	360	6	ABU80447	Abu80447 Human PRO
44	857.5	46.2	360	6	ABO01811	Abo01811 Novel hum
45	857.5	46.2	360	6	ABR99365	Abr99365 Human sec

ALIGNMENTS

RESULT 1
ADM87304
ID   ADM87304 standard; protein; 340 AA.
XX
AC   ADM87304;
XX
DT   03-JUN-2004 (first entry)
XX
DE   Human protein SEQ ID NO:397.
XX
KW   respiratory; cytostatic; antiarthritic; antinflammatory;
KW   gastrointestinal; antibacterial; immunosuppressive; antidiabetic;
KW   antirheumatic; gene therapy; molecular weight marker; chromosome marker;
KW   chromosome tag; genetic fingerprinting; nutritional supplement; cancer;
KW   inflammatory condition; arthritis; inflammatory bowel disease;
KW   Crohn's disease; sepsis; rheumatoid arthritis; diabetes mellitus type 1;
KW   graft versus host disease; human.
XX
OS   Homo sapiens.
XX
PN   WO2004009834-A2.
XX
PD   29-JAN-2004.
XX
PF   19-JUL-2002; 2002WO-US022858.
XX
PR   21-JUL-2001; 2001US-0306971P.
PR   28-MAR-2002; 2002US-0112944.
XX
PA   (NUVB-) NUVELO INC.
XX
PI   Tang YT, Yang Y, Weng G, Zhang J, Ren F, Xue A, Wang J;
PI   Wehrman T, Ghosh MJ, Wang D, Zhao QA, Wang Z;
XX
DR   WPI; 2004-143291/14.
DR   N-PSDB; ADM87060.
XX
PT   New isolated polynucleotides and polypeptides, useful for treating, e.g.
PT   cancer, lung or liver fibrosis, arthritis, inflammatory bowel disease,
PT   Crohn's disease, rheumatoid arthritis, diabetes mellitus type 1 or graft
PT   versus host disease.
XX
PS   Claim 20; SEQ ID NO 397; 591pp; English.
XX
CC   The present invention describes an isolated polynucleotide (I): (a)
CC   comprising a nucleotide sequence selected from SEQ ID NO:1-244; or (b)
CC   which encodes a polypeptide with biological activity, where the

```
              GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on:    February 10, 2006, 16:23:55 ; Search time 43 Seconds
                            (without alignments)
                    763.021 Million cell updates/sec

Title:         US-10-613-076-48
Perfect score: 1857
Sequence:      1 MPGWLTLPTLCRFLLWAFTI..........FGPPRPQQAAYGXXCYAENX 341

Scoring table: BLOSUM62
               Gapop 10.0 , Gapext 0.5

Searched:      283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters:      283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :    PIR_80:*
              1: pir1:*
              2: pir2:*
              3: pir3:*
              4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                          SUMMARIES
```

Result No.	Score	Query Match %	Length	DB	ID	Description
1	1856	99.9	340	2	JC7505	brain link protein
2	811.5	43.7	354	1	LKHU	proteoglycan link
3	799	43.0	355	1	LKCH	proteoglycan link
4	798	43.0	408	1	LKRT2	proteoglycan link
5	795.5	42.8	354	1	S04243	proteoglycan link
6	788.5	42.5	354	1	S42938	proteoglycan link
7	579	31.2	1268	2	S52781	neurocan - mouse
8	576.5	31.0	1257	2	S28764	neurocan precursor
9	550	29.6	912	2	A54423	brevican precursor
10	546.5	29.4	378	2	I46268	brevican precursor
11	533.5	28.7	3562	2	A47171	chondroitin sulfat
12	533	28.7	371	2	A53908	brevican precursor
13	529.5	28.5	883	2	S49126	brevican precursor
14	528.5	28.5	883	2	S57653	brevican precursor
15	522	28.1	2415	2	A39086	aggrecan precursor
16	517	27.8	2409	1	A60979	versican precursor
17	509	27.4	2132	1	A55182	aggrecan precursor
18	508	27.4	2327	2	T42630	aggrecan - bovine
19	506.5	27.3	1643	2	T14274	versican precursor
20	506.5	27.3	3381	2	T42389	versican precursor
21	506	27.2	2397	2	S29139	aggrecan - pig (fr
22	503.5	27.1	2397	1	A55535	versican precursor
23	502	27.0	2124	2	A28452	proteoglycan core
24	495.5	26.7	2109	1	I50421	aggrecan precursor
25	357	19.2	1340	2	A39808	proteoglycan core
26	253.5	13.7	862	2	S43922	versican - pig-tai
27	204.5	11.0	275	2	JC6506	tumor necrosis fac
28	203.5	11.0	276	2	A47290	TSG-6 homolog PS4
29	192.5	10.4	277	2	A41735	hyaluronate-bindin
30	183.5	9.9	113	2	A55885	chondroitin sulfat
31	170	9.2	1069	2	T42681	hypothetical prote
32	164.5	8.9	101	2	A29165	proteoglycan link
33	125	6.7	943	2	B45082	neurotrophic recep
34	107.5	5.8	468	2	D83218	hypothetical prote
35	104.5	5.6	117	2	LVHU2	Ig lambda chain pr
36	104.5	5.6	117	2	S04526	Ig lambda chain pr
37	104.5	5.6	120	2	S30528	Ig lambda chain V
38	104	5.6	919	2	T32541	unc-5 protein - Ca
39	104	5.6	947	1	B44294	unc-5 protein, lon
40	104	5.6	1694	2	S50065	sialoadhesin - mou
41	102.5	5.5	98	2	S36063	Ig lambda chain -
42	102	5.5	1323	2	PN0568	connectin 3B - chi
43	102	5.5	4391	2	A38096	perlecan precursor
44	101	5.4	769	1	QRRTGS	secretory componen
45	100	5.4	235	2	S25749	Ig lambda chain -

ALIGNMENTS

```
RESULT 1
JC7505
brain link protein-1 - human
C;Species: Homo sapiens (man)
C;Date: 17-Nov-2000 #sequence_revision 17-Nov-2000 #text_change 09-Jul-2004
C;Accession: JC7505
R;Hirakawa, S.; Oohashi, T.; Su, W.D.; Yoshioka, H.; Murakami, T.; Arata, J.; Ninomiya
Biochem. Biophys. Res. Commun. 276, 982-989, 2000
A;Title: The brain link protein-1 (BRAL1): cDNA cloning, genomic structure, and charac
A;Reference number: JC7505
A;Accession: JC7505
A;Molecule type: mRNA
A;Residues: 1-340 <HIR>
A;Cross-references: UNIPROT:O9GZV7; UNIPARC:UPI00000012E0; DDBJ:AB049054
C;Comment: This protein stabilizes the binding between hyaluronan and brain-specific h
A;Genetics:
A;Gene: brall
C;Superfamily: proteoglycan link protein; immunoglobulin homology; link protein repeat
C;Keywords: brain; tandem repeat

Query Match          99.9%;    Score 1856;   DB 2;   Length 340;
Best Local Similarity 99.4%;   Pred. No. 6.2e-144;
Matches 338;   Conservative 0;   Mismatches 2;   Indels 0;   Gaps 0;

Qy    1 MPGWLTLPTLCRFLLWAFTIPHKAQGDPASHPGPHYLLPPIHEVIHSHRGATATLPCVLG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 MPGWLTLPTLCRFLLWAFTIPHKAQGDPASHPGPHYLLPPIHEVIHSHRGATATLPCVLG 60

Qy   61 TTPPSYKVRWSKVEPGELRETLILITNGLHARGYGPLGGRARMRRGHRLDASLVIAGVRL 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 TTPPSYKVRWSKVEPGELRETLILITNGLHARGYGPLGGRARMRRGHRLDASLVIAGVRL 120

Qy  121 EDEGRYRCELINGIEDESVALTLSLEGVVFPYQPSRGRYQFNYYEAKQACEBQDGRLATY 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 EDEGRYRCELINGIEDESVALTLSLEGVVFPYQPSRGRYQFNYYEAKQACEBQDGRLATY 180

Qy  181 SQLYQAWTEGLDWCNAGWLLBGSVRYPVLTARAPCCGRGRPGIRSYGPRDRMRDRYDAFC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 SQLYQAWTEGLDWCNAGWLLBGSVRYPVLTARAPCCGRGRPGIRSYGPRDRMRDRYDAFC 240

Qy  241 FTSALAGQVFPVPGRLTLSRAHAACRRRGAVVAKVGHLYAAWKFSGLDQCDGGWLADGSV 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 FTSALAGQVFPVPGRLTLSRAHAACRRRGAVVAKVGHLYAAWKFSGLDQCDGGWLADGSV 300

Qy  301 RFPITTPRPRCGGLPDPGVRSFGFPRPQQAAYGXXCYAEN 340
          |||||||||| |||||||||||||||||||||||| ||||
Db  301 RFPITTPRPRCGGLPDPGVRSFGFPRPQQAAYGTYCYAEN 340

RESULT 2
LKHU
proteoglycan link protein precursor [validated] - human
```

```
                    GenCore version 5.1.7
          Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on:     February 10, 2006; 16:20:24 ; Search time 254 seconds
                                           (without alignments)
                               947.186 Million cell updates/sec

Title:      US-10-613-076-48
Perfect score:  1857
Sequence:   1 MPGWLTLPTLCRFLLWAFTI.........FGFPRPQOAAYGXXCYAENX 341

Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched:       2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters:       2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :      UniProt 05.80:*
                1: uniprot_sprot:*
                2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                        SUMMARIES
```

Result No.	Score	Query Match %	Length	DB	ID	Description
1	1856	99.9	340	1	HPLN2_HUMAN	Q9gzv7 homo sapien
2	1856	99.9	340	2	Q5T3J0_HUMAN	Q5t3j0 homo sapien
3	1693.5	91.2	341	1	HPLN2_RAT	Q9esm2 rattus norv
4	1690.5	91.0	341	1	HPLN2_MOUSE	Q9esm3 mus musculu
5	1000	53.9	185	2	Q5T3J1_HUMAN	Q5t3j1 homo sapien
6	895	48.2	386	2	Q4S472_TETNG	Q4s472 tetraodon n
7	857.5	46.2	360	1	HPLN3_HUMAN	Q96886 homo sapien
8	850.5	45.8	383	2	Q5BJ60_XENTR	Q5bj60 xenopus tro
9	848	45.7	359	2	Q5R1X6_RAT	Q5r1x6 rattus norv
10	848	45.7	394	2	Q6DCI6_XENLA	Q6dci6 xenopus lae
11	837	45.1	359	2	Q7ZX17_XENLA	Q7zx17 xenopus lae
12	834	44.9	359	1	HPLN3_MOUSE	Q80wm5 mus musculu
13	811.5	43.7	354	1	HPLN1_HUMAN	P10915 homo sapien
14	805.5	43.4	363	2	Q6NV41_BRARE	Q6nv41 brachydanio
15	799	43.0	355	1	HPLN1_CHICK	P07354 gallus gall
16	795.5	42.8	354	1	HPLN1_PIG	P10859 sus scrofa
17	795	42.8	313	2	Q4SHL9_TETNG	Q4shl9 tetraodon n
18	792.5	42.7	356	1	HPLN1_MOUSE	Q9qup5 mus musculu
19	791.5	42.6	354	1	HPLN1_RAT	P03994 rattus norv
20	789.5	42.5	354	1	HPLN1_BOVIN	P55252 bos taurus
21	789	42.5	314	2	Q4SB78_TETNG	Q4sb78 tetraodon n
22	788.5	42.5	319	2	Q4S1V7_TETNG	Q4s1v7 tetraodon n
23	788.5	42.5	354	1	HPLN1_HORSE	Q28381 equus cabal
24	768	41.4	400	1	HPLN4_MOUSE	Q80wm4 mus musculu
25	744.5	40.1	402	1	HPLN4_HUMAN	Q86uw8 homo sapien
26	714	38.4	335	2	Q60H44_BRARE	Q60h44 brachydanio
27	698	37.6	889	2	Q4RUP0_TETNG	Q4rup0 tetraodon n
28	579	31.2	1268	1	CSPG3_MOUSE	P55066 mus musculu
29	576.5	31.0	1257	1	CSPG3_RAT	P55067 rattus norv
30	568.5	30.6	1321	1	CSPG3_HUMAN	O14594 homo sapien
31	568.5	30.6	1335	2	Q4LE67_HUMAN	Q4le67 homo sapien
32	566	30.5	1059	2	Q5ISN4_MACPA	Q5isn4 macaca fasc
33	565.5	30.5	1321	1	CSPG3_PANTR	Q5is41 pan troglod
34	559	30.1	1570	2	Q75ZI3_BRARE	Q75zi3 brachydanio
35	556.5	30.0	1290	1	Q9W6B1_CHICK	Q9w6e1 gallus gall
36	550	29.6	912	1	PGCB_BOVIN	Q28062 bos taurus
37	546.5	29.4	417	2	PGCB_FELCA	P41725 felis silve
38	545	29.3	1441	2	Q4S3C4_TETNG	Q4s3c4 tetraodon n
39	543	29.2	671	2	Q5T3I5_HUMAN	Q5t3i5 homo sapien
40	543	29.2	911	1	PGCB_HUMAN	Q96gw7 homo sapien
41	543	29.2	911	2	Q5SZI0_HUMAN	Q5szi0 homo sapien
42	536.5	28.9	883	2	Q80WT7_MOUSE	Q80wt7 mus musculu
43	536	28.9	2586	1	Q4RUP1_TETNG	Q4rup1 tetraodon n
44	533.5	28.7	3562	1	CSPG2_CHICK	Q90953 gallus gall
45	530.5	28.6	850	2	Q59F90_HUMAN	Q59f90 homo sapien

```
                        ALIGNMENTS

RESULT 1
HPLN2_HUMAN
ID   HPLN2_HUMAN     STANDARD;      PRT;     340 AA.
AC   Q9GZV7;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Hyaluronan and proteoglycan link protein 2 precursor (Brain link
DE   protein 1).
GN   Name=HAPLN2; Synonyms=BRAL1;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE, AND TISSUE SPECIFICITY.
RX   MEDLINE=20483618; PubMed=11027579; DOI=10.1006/bbrc.2000.3583;
RA   Hirakawa S., Oohashi T., Su W.-D., Yoshioka H., Murakami T., Arata J.,
RA   Ninomiya Y.;
RT   "The brain link protein-1 (BRAL1); cDNA cloning, genomic structure,
RT   and characterization as a novel link protein expressed in adult
RT   brain.";
RL   Biochem. Biophys. Res. Commun. 276:982-989(2000).
RN   [2]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC   TISSUE=Brain;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.B.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC   -!- FUNCTION: Mediates a firm binding of versican V2 to hyaluronic
CC       acid. May play a pivotal role in the formation of the hyaluronan-
CC       associated matrix in the central nervous system (CNS) which
CC       facilitates neuronal conduction and general structural
CC       stabilization. Binds to hyaluronic acid (By similarity).
CC   -!- SUBCELLULAR LOCATION: Secreted; extracellular matrix (By
```